

EXHIBIT 1

Amino acid sequence of insert of Plasmid M15pREP (pQE-Ct-Uni) #37.

MRGSHHHHHGSACELGTPGRRVPDPTKESLSNKISLTGDTHNLTNCYLDNLRYILAIL
QKTPNEGAAVTIDYLSSFFDTQKEGIYFAKNLTPESGGAIYGASPNSPTVEIRDTIGPV
IFENNTCCRPFSSNPNAVNKIREGGAIHAQONLYINHNHDVVGFMKNFSYVRGGAIST
ANTFVVSENQSCFLFMDNICIQTNTAGKGGAIYAGTSNSFESNNCDLFFINNACCAGGA
IFSPICSLTGNRGNIVFYNNRCFKNVTASSEASDGGAIKVTRLDVTGNRGRIFFSDN
ITKNYGGAIYAPVVTLDNGPTYFINNVANNKGAIYIDGTSNSKISADRHAIIFNENI
VTNVTSANGTSTSANPPRNAITVASSSGEILLGAGSSQNLIFYDPIEVSNAGVSFSN
KEADQTGSVVFSGATVNSADFQQRNLQTKTPAPLTLNGFLCIEDHAQLTVNRFTQTGG
VVSLGNGAVLSCYKNGAGNSASNITLKHIGLNSSILKSGAEIPLLWVEPTNNSNY
TADTAATFSLSDVKLSLIDDYGNSPYESTDLTHALSSQPMLSISEASDNQLRSDDMDFS
GLNVPHYGWQGLWSWGWAQTQDPEPASSATIDPKKANRFHRTLLLWLPAGYVPSPKH
RSPLIANTLWGNMLLATESLKNSAELTPSDHPFWGITGGGLGMMVQEPRENHPGFHMR
SSGYFAGMIAGQTHTFSLKSQTYTKLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLAK
LVGLYSYGDHNCHFYTQGENLTSQGTFRSQTMGGAVFFDLPMKPFGSTHILTAPFLGA
LGIYSSLSHFTEVGAYPRSFSTKTPINVLPVIGVKGSFMNATQRPOAWTVELAYQPVL
YRQELEIATQLLASKGIWFGSGSPSSRHAMSYKISQQTQPLSWLTLHFQYHGFYSSSTF
CNYLNGEIALRF.

Nucleic acid sequence of Plasmid M15pREP (pQE-Ct-Uni) #37.

ATGAGAGGATCGCATCACCATCACCATCACGGATCCGATCGAGCTCGGTACCCGGGTC
GACGGGTTCCAGATCCTACGAAAGAGTCGCTATCAAATAAAATTAGTTGACAGGAGACAC
TCACAATCTCACTAACTGCTATCTGATAACCTACGCTACATACTGGCTATTCTACAAAAAA
CTCCAATGAAGGAGCTGCTGTCACAATAACAGATTACCTAAGCTTTTGATAACACAAAAA
AGAAGGTATTATTGCAAAAATCTCACCCCTGAAAGTGGTGGTGCATTGGTATGCG
AGTCCAATTCTCCTACCGTGGAGATTGTGATAACAATAGGTCTGTAATCTTGAAAATAA
TACTTGTGCAGACCATTACATCGAGTAATCTTAATGCAGCTGTTAATAAAATAAGAGAA
GGCGGAGCCATTATGCTAAAATCTTACATAATCACAATCATGATGTGGTCGGATTAT
GAAGAACTTTCTTATGTCCGAGGAGGCCATTAGTACCGCTAACACCTTGTGAGCG
AGAATCAGCTTGTCTTCTTATGGACAACATCTGTATTCAAACATAACAGCAGGAAA
GGTGGCGCTATCTATGCTGGAACGAGCAATTCTTGAGAGTAATAACTCGATCTCTT
TATCAATAACGCCGTGTGCAAGGAGGAGCGATCTCTCCCTATCTGTTCTAAACAGGAA
ATCGTGGTAACATCGTTCTATAACAATCGCTGCTTAAAAATGTAGAAACAGCTCTCA
GAAGCTTGTGATGGAGGAGCAATTAAAGTAACACTCGCCTAGATGTACAGGCAATCGT
GTAGGATCTTTAGTACAATACACAAAAATTATGGCGGAGCTTTACGCTCTGTA

GTTACCCTAGTGGATAATGGCCCTACCTACTTTATAAACAATGTCGCCAATAATAAGGGGG
GCGCTATCTATATAGACGGAACCGAGCAACTCCAAAATTCTGCCGACCGCCATGCTATTATT
TTAATGAAAATATTGTGACTAATGTAACTAGTCAAATGGTACCGAGTCAGCTAATC
CTCCTAGAAGAAATGCAATAACAGTAGCAAGCTCTGGTCAAATTCTATTAGGAGCAGG
GAGTAGCCAAAATTAAATTCTATTGATCCTATTGAAGTTAGCAATGCAGGGGTCTGTGT
CCTCAATAAGGAAGCTGATCAAACAGGCTCTGTAGTATTTCAGGAGCTACTGTTAATTCT
GCAGATTTCATCAACGCAATTACAAACAAAAACACCTGCACCCCTACTCTCAGTAATG
GTTTCTATGTATCGAAGATCATGCTCAGTTACAGTGAATCGATTACACACAAACTGGGGT
GTTGTTCTCTGGGAATGGAGCAGTCTGAGTTGCTATAAAATGGTGCAGGAAATTCTGC
TAGCAATGCCTCTATAACACTGAAGCATATTGGATTGAATCTTCTTCATTGAAAAGTG
GTGCTGAGATTCTTATTGTGGGTAGAGCCTACAAATAACAGCAATAACTATACAGCAGA
TACTGCAGCTACCTTCAATTAAAGTGTGAAAATCTCACTCATTGATGACTATGGGAATT
CTCCTTATGAATCCACAGATCTAACCCATGCTCTGTCTCACAGCCTATGCTATCTATTCT
GAGGCTAGTGTAAACCAGCTAACAGATCTGATGATATGGATTCTCGGGACTAAATGTCCCTC
ATTATGGATGGCAAGGACTTTGGAGTTGGGCTGGCAAAAATCAAGATCCAGAACCAAG
CATCTTCAGCAACAATCACAGATCCAAAAAGCCAATAGATTCCATAGAACCTTATTACT
GACTTGGCTTCTGCTGGGTATGTTCTAGCCCACAGAACAGAAGTCCCCTCATAGCGAAT
ACCTTATGGGGGAATATGCTGCTGCAACAGAAAGCTTAAAAAATAGTCAGAACTGACAC
CTAGTGTATCCTTCTGGGAATTACAGGAGGAGACTAGGCATGATGGTTACCAAGA
ACCTCGAGAAAATCATCCTGGATTCCATATGCGCTCTCCGGATACTTGCGGGATGATA
GCAGGGCAAACACATACCTCTCATTGAAATTCACTGAGACCTACACCAAACATGAGC
GTTACGAAAAAACACGTATCTCTAAAATTACTCATGCCAAGGAGAAATGCTCTCTC
ATTGCAAGAAGGTTCTGCTGGCTAAATTAGTTGGCTTACAGCTATGGAGATCATAACT
GTCACCATTCTATACCCAAAGGAGAAAATCTAACATCTCAAGGGACGTTCCGTAGTC
GATGGGAGGTGCTGTTTTGATCTCCCTATGAAACCCCTTGGATCAACGCATATACTGA
CAGCTCCCTTTAGGTGCTCTGGTATTCTAGCCTGTCTCACTTACTGAGGTGGAG
CCTATCCCGCGAAGCTTCTACAAAGACTCCTTGATCAATGCTCTAGTCCCTATTGGAGTT
AAAGGTAGCTTATGAATGCTACCCAAAGACCTCAAGCCTGGACTGTAGAATTGGCATACC
AACCCGTTCTGTATAAGACAAGAACTAGAGATCGCGACCCAGCTCTAGCCAGTAAAGGTAT
TTGGTTGGTAGTGGAAAGCCCTCATCGCGTCAATGCCATGTCCTATAAAATCTCACAGCAA
CACAAACCTTGAGTTGGTAACTCTCCATTCCAGTATCATGGATTCTACTCCTCTAACCT
TCTGTAATTCTCAATGGGGAAATTGCTCTCGGATCTAA



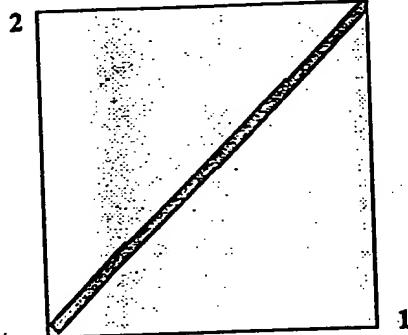
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix **BLOSUM62** | gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** Filter Align

Sequence 1 **lcl|seq_1** Length 956 (1 .. 956)

Sequence 2 **lcl|seq_2** Length 965 (1 .. 965)



NOTI (bit score and expect value) is calculated based on the size of nr database

Score = 1885 bits (4884), Expect = 0.0
 Identities = 925/934 (99%), Positives = 930/934 (99%)

Query: 23 VPDPTKESLSNKISLTGDTNLTNCYLQKTPNEGAUTITDYLSSFFDTQK 82
 VPDPTKESLSNKISLTGDTNLTNCYLQKTPNEGAUTITDYLSSFFDTQK 91
 Sbjct: 32 VPDPTKESLSNKISLTGDTNLTNCYLQKTPNEGAUTITDYLSSFFDTQK 142
 EGIYFAKNLTPESGGAIGYASPNSPTVEIRD TIGPVIFENNTCCRPTSSNPNAAVNKIR
 EGIYFAKNLTPESGGAIGYASPNSPTVEIRD TIGPVIFENNTCCRPTSSNPNAAVNKIR 151
 Sbjct: 92 EGIYFAKNLTPESGGAIGYASPNSPTVEIRD TIGPVIFENNTCCRPTSSNPNAAVNKIR 202
 EGGAIHAQNLINYHNHDVVGFMKNFSYVRGGAISTANTFVSENQSCFLFMDNICIQTNT
 EGGAIHAQNLINYHNHDVVGFMKNFSYVRGGAISTANTFVSENQSCFLFMDNICIQTNT 211
 Sbjct: 152 EGGAIHAQNLINYHNHDVVGFMKNFSYVRGGAISTANTFVSENQSCFLFMDNICIQTNT 262
 AGKGGAIIYAGTSNSFESNNCDLFFINNACCAGGAIFSPICSLTGNGRNIVFYNRCKNV
 AGKGGAIIYAGTSNSFESNNCDLFFINNACCAGGAIFSPICSLTGNGRNIVFYNRCKNV 271
 Sbjct: 212 AGKGGAIIYAGTSNSFESNNCDLFFINNACCAGGAIFSPICSLTGNGRNIVFYNRCKNV 322
 ETASSEASDGGAIKVTRLDVTGNRGRIFFSNDITKNYGGAIYAPVVTLVONGPTYFINN
 ETASSEASDGGAIKVTRLDVTGNRGRIFFSNDITKNYGGAIYAPVVTLVONGPTYFINN 331
 Sbjct: 272 ETASSEASDGGAIKVTRLDVTGNRGRIFFSNDITKNYGGAIYAPVVTLVONGPTYFINN 382
 VANNKGGAIYIDGTSNSKISADRHAIIFNENIVTNVTSA NGTSTSANPPRNNAITVASSS
 +ANNKGGAIYIDGTSNSKISADRHAIIFNENIVTNVT+ANGTSTSANPPRNNAITVASSS
 Sbjct: 332 IANNKGGAIYIDGTSNSKISADRHAIIFNENIVTNVTNANGTSTSANPPRNNAITVASSS 391
 Query: 383 GEILLGAGSSQNLIFYDPIEVSNAGVSFSNKEADQTSVVFSGATVNSADFHQRNLQTK 442
 GEILLGAGSSQNLIFYDPIEVSNAGVSFSNKEADQTSVVFSGATVNSADFHQRNLQTK 451
 Sbjct: 392 GEILLGAGSSQNLIFYDPIEVSNAGVSFSNKEADQTSVVFSGATVNSADFHQRNLQTK 502
 TPAPLTLNGFLCIEDHAQLTVNRFQTGGVSLGNGAVLSCYKNGAGNSASNASITLKH
 TPAPLTLNGFLCIEDHAQLTVNRFQTGGVSLGNGAVLSCYKNGAGNSASNASITLKH 511
 Sbjct: 452 TPAPLTLNGFLCIEDHAQLTVNRFQTGGVSLGNGAVLSCYKNGAGNSASNASITLKH 562
 Query: 503 IGLNLSSILKSGAEIPLLWVEPTNNNNYTADTAATPSLSDVKLSLIDDYGNSPYESTDL
 IGLNLSSILKSGAEIPLLWVEPTNNNNYTADTAATPSLSDVKLSLIDDYGNSPYESTDL

Blast Result

today, September 6, 2001

bjct: 512 IGLNLSSILKSGAEIPLLWEPINNSNNYTADTAATFSLSDVKLSLIDDYGNSPYESTDL 571
 query: 563 THALSSQPMILSISEASDNQLRSDDMDFSGLNVPHYGWQGLWSWGWAQTQDPEPASSATIT 622
 THALSSQPMILSISEASDNQLRSDDMDFSGLNVPHYGWQGLW+WGWAQTQDPEPASSATIT 631
 bjct: 572 THALSSQPMILSISEASDNQLRSDDMDFSGLNVPHYGWQGLWTWGWAQTQDPEPASSATIT 682
 query: 623 DPKKANRFHRTLLLTLWPAGYVPSPKHRSPLIANTLWGNMLLATESLKNSAELTPSDHFF 691
 DP+KANRFHRTLLLTLWPAGYVPSPKHRSPLIANTLWGNMLLATESLKNSAELTPSDHFF 691
 bjct: 632 DPQKANRFHRTLLLTLWPAGYVPSPKHRSPLIANTLWGNMLLATESLKNSAELTPSDHFF 691
 Query: 683 WGITGGGLGMMVYQEPRENHPGFHMRSSSGYFAGMIAGQHTFSLKFQSQTYTKLNERYAKN 742
 WGITGGGLGMMVYQ+PRENHPGFHMRSSSGY AGMIAGQHTFSLKFQSQTYTKLNERYAKN 751
 Sbjct: 692 WGITGGGLGMMVYQDPRENHPGFHMRSSSGYAGMIAGQHTFSLKFQSQTYTKLNERYAKN 802
 Query: 743 NVSSKNYSCQGEMLFSLQEGFLAKLVGLYSYGDHNCHHFYTQGENLTSQGTFRSQTMMGG 802
 NVSSKNYSCQGEMLFSLQEGFL KLVGLYSYGDHNCHHFYTQGENLTSQGTFRSQTMMGG 811
 Sbjct: 752 NVSSKNYSCQGEMLFSLQEGFLTKLVGLYSYGDHNCHHFYTQGENLTSQGTFRSQTMMGG 811
 Query: 803 AVFFDLPMPKPGSTHILTAFLGALGIYSSLSHFTEVGAYPRSFSTKPLINVLPVGK 862
 AVFFDLPMPKPGSTHILTAFLGALGIYSSLSHFTEVGAYPRSFSTKPLINVLPVGK 871
 Sbjct: 812 AVFFDLPMPKPGSTHILTAFLGALGIYSSLSHFTEVGAYPRSFSTKPLINVLPVGK 871
 Query: 863 GSFMNATQRQPQAWTVELAYQPVLYRQELEIATQLLASKIWFSGSGPSSRHAMSYKISQQ 922
 GSFMNATQRQPQAWTVELAYQPVLYRQE IATQLLASKIWFSGSGPSSRHAMSYKISQQ 931
 Sbjct: 872 GSFMNATQRQPQAWTVELAYQPVLYRQEPEGIATQLLASKIWFSGSGPSSRHAMSYKISQQ 956
 Query: 923 TQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF 956
 TQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF 965
 Sbjct: 932 TQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF 965

CPU time: 0.36 user secs. 0.02 sys. secs 0.38 total secs.

Gapped
 Lambda K H
 0.316 0.132 0.396

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 12,524
 Number of Sequences: 0
 Number of extensions: 873
 Number of successful extensions: 15
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 1
 length of query: 956
 length of database: 239,316,239
 effective HSP length: 131
 effective length of query: 825
 effective length of database: 206,523,009
 effective search space: 170381482425
 effective search space used: 170381482425
 T: 9
 A: 40
 X1: 16 (7.3 bits)
 X2: 129 (49.7 bits)
 X3: 129 (49.7 bits)
 S1: 41 (21.6 bits)
 S2: 77 (34.3 bits)